

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: March 17, 2004, 18:47:23 ; Search time 25.0763 Seconds

(without alignments) 6683.183 Million cell updates/sec

Title: Score: 3326 US-09-989-981A-6

Sequence: 1 MGDLSSLTPOGGSMGLQVNRRG... PALVILGIVVFKIRDHLSR 651

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/us07_pubcomb.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTRS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/us08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/us10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/us10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/us60_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/us60_pubcomb.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	3326	100.0	651	9 US-09-987-992-3	Sequence 3, Appli
2	3326	100.0	651	10 US-09-989-981A-6	Sequence 6, Appli
3	3326	100.0	651	14 US-10-090-455-6	Sequence 1, Appli
4	2744.5	82.5	652	9 US-09-837-992-1	Sequence 2, Appli
5	2744.5	82.5	652	10 US-09-989-981A-2	Sequence 2/5, Appli
6	1308	39.3	256	15 US-10-104-279-95	Sequence 4, Appli
7	697	21.0	672	10 US-09-989-981A-4	Sequence 5, Appli
8	697	21.0	673	10 US-09-989-981A-8	Sequence 6, Appli
9	697	21.0	673	14 US-10-090-455-7	Sequence 7, Appli
10	682.5	20.5	655	10 US-09-961-086-1	Sequence 1, Appli
11	682.5	20.5	655	15 US-10-405-806-13	Sequence 1/3, Appli
12	680.5	20.5	655	9 US-09-981-353-35	Sequence 3/5, Appli
13	680.5	20.5	655	14 US-10-120-687-61	Sequence 6/1, Appli
14	680.5	20.5	655	15 US-10-405-806-2	Sequence 2, Appli
15	674.5	20.3	655	9 US-09-866-866A-10	Sequence 10, Appli

ALIGNMENTS

SEQ ID NO	LENGTH	TYPE	ORGANISM	FEATURE	OTHER INFORMATION	OTHER INFORMATION: amino acid sequence
3	651	PRT	Homo sapiens			US-09-837-992-3
4	651	PRT				
5	651	PRT				
6	651	PRT				
7	652	PRT				
8	672	PRT				
9	673	PRT				
10	655	PRT				
11	655	PRT				
12	655	PRT				
13	655	PRT				
14	655	PRT				
15	655	PRT				

Query 1 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 2 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 3 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 4 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 5 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 6 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 7 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 8 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 9 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 10 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 11 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 12 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 13 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 14 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 15 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 16 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 17 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 18 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 19 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 20 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 21 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 22 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 23 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 24 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 25 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 26 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 27 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 28 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 29 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 30 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 31 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 32 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 33 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 34 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 35 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 36 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 37 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 38 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 39 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 40 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 41 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 42 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 43 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 44 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Query 45 MGDLSSLTPOGGSMGLQVNRRGQSSELEGAPATAPEPHS

Sequence 5, Appl	Sequence 27, Appl
Sequence 14, Appl	Sequence 2025, AP
Sequence 1120, AP	Sequence 54421, A
Sequence 17591, AP	Sequence 16182, AP
Sequence 215, AP	Sequence 4, Appl
Sequence 10, Appl	Sequence 10, Appl
Sequence 5547, AP	Sequence 9, Appl
Sequence 10, Appl	Sequence 2, Appl
Sequence 6125, A	Sequence 8, Appl
Sequence 244078, AP	Sequence 197, APP
Sequence 6125, A	Sequence 1, APP
Sequence 4, Appl	Sequence 15459, AP
Sequence 13, Appl	Sequence 14, Appl
Sequence 8, Appl	Sequence 5740, AP
Sequence 5748, AP	Sequence 218651, AP
Sequence 53346, A	Sequence 64380, A
Sequence 45	
0	
9	
841	
80	

RESULT 4

US-09-837-992-1

Sequence 1: Application US/09837992

Patent No. US20020091687A1

GENERAL INFORMATION:

APPLICANT: Tularik Inc.

APPLICANT: Tian, Hui

APPLICANT: Shan, Bei

APPLICANT: Schultz, Joshua

APPLICANT: Tularik Inc.

TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG): Compositions and Methods of Use

FILE REFERENCE: 018781-007320US

CURRENT APPLICATION NUMBER: US/09/837,992

CURRENT FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: US 60/198,465

PRIOR FILING DATE: 2000-04-18

PRIOR APPLICATION NUMBER: US 60/204,234

PRIOR FILING DATE: 2000-05-15

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 652

TYPE: PRT

ORGANISM: Mus musculus

FEATURE: OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG)

OTHER INFORMATION: amino acid sequence

US-09-837-992-1

RESULT 5

US-09-989-981A-2

Sequence 2: Application US/0989981A

Publication No. US20030049730A1

GENERAL INFORMATION:

APPLICANT: Hobbs, Helen H.

APPLICANT: Shan, Bei

APPLICANT: Barnes, Robert

APPLICANT: Tian, Hui

APPLICANT: Tularik Inc.

APPLICANT: Board of Regents, The University of Texas System

TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use

FILE REFERENCE: 018781-007320US

CURRENT APPLICATION NUMBER: US/09/989,981A

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/253,645

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 652

TYPE: PRT

ORGANISM: Mus musculus

FEATURE: OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG)

OTHER INFORMATION: amino acid sequence

US-09-837-992-1

Query Match Similarity: 80.2%; Score: 2744.5; DB: 9; Length: 652; Best Local Similarity: 80.2%; Pred. No: 8.8e-254; Matches: 523; Conservative: 64; Mismatches: 64; Indels: 1; Gaps: 1;

QY 1 MGDLISLPGGSGMLOVGRGSSOSSLEGAPATEP-HSLGILHASVSHRVRPWDIT 59

Db 1 MGELPFISPEGARPHPRHGRGSSLSSIEQGSVIGTEARHSLGVHVSNSVRGPWNKIS 60

QY 60 CROWQTREILKDVLSYVSGQMCILGSSGSKTTLADMSGRGLGRAGTFLGEVYNGRA 119

Db 61 CRRQFQOCFSYVQLOSPDLISSTVRELYTIALAARRGNGSFORKVEAMWAEILSHV 180

QY 121 RRBOFQOCFSYVQLOSPDLISSTVRELYTIALAARRGNGSFORKVEAMWAEILSHV 180

Db 181 ADRLGWYSLGGTSTGERRRSTAQQLQDPKMLDEPTGLDCMTANQIVVULVELAR 240

QY 181 ADRLGWYSLGGTSTGERRRSTAQQLQDPKMLDEPTGLDCMTANQIVVULVELAR 240

Db 181 ADRLGWYSLGGTSTGERRRSTAQQLQDPKMLDEPTGLDCMTANQIVVULVELAR 240

QY 241 RNRIVVLTITHQPSLELQFDKIALSFGELIFCGTPAEMIDFFNNDGCPCEHSNPFDF 300

Db 241 RNRIVVLTITHQPSLELQFDKIALSFGELIFCGTPAEMIDFFNNDGCPCEHSNPFDF 300

QY 301 YMFLTSVDTQSREKETTSKRYQOMISAYKSAICHTKLKINTERMCHKLTKLPMVFKTKD 360

Db 301 YMFLTSVDTQSREKETTSKRYQOMISAYKSAICHTKLKINTERMCHKLTKLPMVFKTKD 360

QY 361 SPGVFSKLGVLVLRVTRNLVNLKAVTRLQLNGLFLPVLAVRSNVLKGAIQDRV 420

Db 361 SPGVFSKLGVLVLRVTRNLVNLKAVTRLQLNGLFLPVLAVRSNVLKGAIQDRV 420

QY 361 SPGVFSKLGVLVLRVTRNLVNLKAVTRLQLNGLFLPVLAVRSNVLKGAIQDRV 420

Db 421 GLYQFVGAATPGMMLAVNLFLPVLAVSDQSGLYQKOMMLAYALHVLPSVATM 480

Db 421 GLYQFVGAATPGMMLAVNLFLPVLAVSDQSGLYQKOMMLAYALHVLPSVATM 480

QY 481 IISVSVCTTGLHPEVARFVGYSAALLAAPHLTGEFLTIVLGIQVNPNTIVSVALSIA 540

Db 481 IISVSVCTTGLHPEVARFVGYSAALLAAPHLTGEFLTIVLGIQVNPNTIVSVALSIA 540

QY 481 IISVSVCTTGLHPEVARFVGYSAALLAAPHLTGEFLTIVLGIQVNPNTIVSVALSIA 540

Db 481 IISVSVCTTGLHPEVARFVGYSAALLAAPHLTGEFLTIVLGIQVNPNTIVSVALSIA 540

QY 541 GIVVNGSGLIRNQEMPPFKLISYFTQKYSBILVNEFVQGLNFTCGSSANSVTNPNC 600

Db 541 GIVVNGSGLIRNQEMPPFKLISYFTQKYSBILVNEFVQGLNFTCGSSANSVTNPNC 600

QY 541 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

Db 541 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

QY 601 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

Db 601 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

QY 600 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

Db 601 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

QY 601 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

Db 601 AFTOGIQFLEKTCPGATSRFTANFLILYSPFIPALVIGIVVFKRDLISR 651

Query Match 82.5%; Score 2744.5; DB 10; Length 652;
 Best Local Similarity 80.2%; Pred. No. 8.8e-254; Indels 1; Gaps 1;
 Matches 523; Conservative 64; Mismatches 64; Del 0; Insert 0; Score 2744.5; DB 10; Length 652;
 Query 1 MGDLSLTPEGSMSGMGLQVNRSQSSLEGAPATAPEP-HSLGILHASYSYSHRNPWMDTS 59
 Db 1 MGELPLFLSPEGARGPHINRGSSLSSLEQGSVITGTEARHSILGVLYSYSVRVGPWNKS 60
 Query 60 CROQWVQQLKDVSYLVSQESQMCIGLSSGSKTLLDAMSGRGRAGFLGTYVNGRA 119
 Db 61 COQKNDQDQIQLKDVSYLVSQESQMCIGLSSGSKTLLDAMSGRGRAGFLGTYVNGRA 119
 Query 120 IRRREQDCSYSYLVSQESQMCIGLSSGSKTLLDAMSGRGRAGFLGTYVNGRA 119
 Db 121 IRRREQDCSYSYLVSQESQMCIGLSSGSKTLLDAMSGRGRAGFLGTYVNGRA 119
 Query 180 VADRLTGNYSIGGISTGERRVSTAQOLQDPKVMLFQDPTGCDMCTANQTVLVELA 239
 Db 181 VADQMGSYNQGIGGERRVSTAQOLQDPKVMLFQDPTGCDMCTANQTVLVELA 240
 Query 240 RNRNLVLTQIOPRSLSFQDKEKILTSFSLIFCGTPAFLDFNDGCPCPERSNPF 299
 Db 241 RDRIVIVTHQPSLSFQDKEKILTSFSLIFCGTPAFLDFNDGCPCPERSNPF 300
 Query 300 FYNMLDLSVPSQKSERIETTSRQWMSATKSAKTSATCKTUNIERNKHKTLPWPKTK 359
 Db 301 FYNMLDLSVPSQKSERIETTSRQWMSATKSAKTSATCKTUNIERNKHKTLPWPKTK 360
 Query 360 DSPGVTSKIGLRLRTRNKLAVITLQLNQMLIGLFLFVVRVSNVKGAIQR 419
 Db 361 DPPGMFGKLGKLYLRRVTRNKLAVITLQLNQMLIGLFLFVVRVSNVKGAIQR 420
 Query 420 VLLVLYQFVGAPYTGMLAVNULPVRAVSQESQDGLQXKQWMLAYALHULPFWAT 479
 Db 421 VLLVLYQFVGAPYTGMLAVNULPVRAVSQESQDGLQXKQWMLAYALHULPFWAT 480
 Query 480 MIFSSVQYWTGQHPEVARFQYFSQALLAFLHIGERLTVLGLTVQPNVNWALIST 539
 Db 481 VIFSSVQYWTGQHPEVARFQYFSQALLAFLHIGERLTVLGLTVQPNVNWALIST 540
 Query 540 AGVIVVESGFLRTOEMIPKKTSYTFQKICSEILVNNFVGLMFTCASSNVSTNM 599
 Db 541 SGUIGSGPFIQIQLQEMIPKKTSYTFQKICSEILVNNFVGLMFTCASSNVSTNM 600
 Query 600 CAFTOGQIQTETKTCGATSRPMTNFIYLVSYTIPALVLTGTVFKARDHLISR 651
 Db 601 GATQGQIQTETKTCGATSRPMTNFIYLVSYTIPALVLTGTVFKARDHLISR 652
 RESULT 6 US-10-104-047-2795
 ; Sequence 2795, Application US/10104047
 ; Publication No. US20030236392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: HI-A105
 ; FILE REFERENCE: 01871-007220US
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIORITY: 2000-11-20
 ; PRIORITY NUMBER: US 60/253,645
 ; PRICE: FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 672
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; OTHER INFORMATION: mouse ABCG8 (mABCg8)
 ; US-09-989-981A-4
 Query Match 21.0%; Score 697; DB 10; Length 672;
 Best Local Similarity 29.1%; Pred. No. 2.2e-116; Indels 84; Gaps 18;
 Matches 195; Conservative 129; Mismatches 263; Del 0; Insert 0; Score 697; DB 10; Length 672;
 Query 15 LQANGRSQSSLEGAPATAPEP-HSLGILHASYSYSHRNPWMDTS 59
 Db 17 LQDASGLQDSL---FSSDSNLYFFSGQSNLTYRDLTYQVDIASQWMEFQLAQPK 72
 Query 62 QWMTQI-----LKVSLVYQESGOMCIGLSSGSKTLLDAMSGRGRAGFLGTYVNGRA 119
 Db 73 IPWASHSSQDSCBGLGIRNLFSKURSGQMLAIGGSSGRASLSDVTRG-GHGKMSQ 131
 Query 113 VVYNGRARRERQFDCSYSYLVSQESQMCIGLSSGSKTLLDAMSGRGRAGFLGTYVNGRA 171
 Db 132 IWINGQPSLQPLVTKCIAHRODQIPLNLTRETAQIQLRPRFQSQAQRDKVEDV 191
 Query 172 MAELSLSHADRLTGNYSIGGISTGERRVSTAQOLQDPKVMLFQDPTGCDMCTANQI 231
 Db 192 TAELRQOCANTRVGNTVQGSGGERVSTAQOLQDPKVMLFQDPTGCDMCTANQI 251
 Query 232 VLLVLYQFVGAPYTGMLAVNULPVRAVSQESQDGLQXKQWMLAYALHULPFWAT 291

Query Match 39.3%; Score 1308; DB 15; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.2e-116; Indels 0; Gaps 0;
 Matches 256; Conservative 0; Mismatches 0; Del 0; Insert 0; Score 1308; DB 15; Length 256;
 US-10-104-047-2795

Db 252 VTIISRLAKGNRILVLIHOPRSIDFLFDLVLIMTSGTPYLGAQMQVYFTSIGHPC 311
 Qy 292 PEISNPDPYMDTSVOTOSKEREIEITSKRVQMEAYKKA-----ICKTLNTERM 345
 Db 312 PRYSNPADPYDVLTSIDRSKEREVATEKAQSLAFLERKQGFDLFLWKAERLNTS 371
 Qy 346 KHKTLPMPFKKDS-----PGFESKCLVLRVTRNLVRNLKAVTRLLQMLNG 397
 Db 372 THWSLTU-----TQDTCGATVELPGNTEQFSTLIRROISHDPRDLTLLHGSEACMS 427
 Qy 398 IFLFPLURVRSVNLKGQDRLQJLQFVSGTPYQMLNANLFLVRAISDQSODGL 457
 Db 428 LITGFLYQHGAKOL-SFMDFAALMIGLIPENVFLDVSKCHERSMVLYYLEDGL 485
 Qy 458 YOKQMMIAYALVLPFSSVATMIFSSCYWTLGHLPEVARGYFSALIAAPHILGBFL- 516
 Db 486 YTAGPYFFAKLGEPLPERCAVYIYAMPIWNLNPVEF----LI-HEILWLV 537
 Qy 517 -----TUVLGTIVONPNT-VNSVWALISIAGVINGSPFLRNUOEMIPPKISYTFQY 570
 Db 538 VFCCTMIALAASAMLPTHMSSFCNALYNFSYLTAGPMILNDNLIVPAWISKSFLR 597
 Qy 571 CSIIUVNVEYGLNFT-CGSSNVSVTNPMACTQIQFETKTCGATSPFMFLY 628
 Db 598 CFFSGLMQIQFNGHLYTTOIGNFTPSILGDTM-----ISAMDLSHPLY 640
 Qy 629 SFPALVILGI 639
 Db 641 ATY--LTWIGI 649

RESULT 8
 US-09-989-981A-8
 ; Sequence 8 Application US/09989981A
 ; Publication No. US20030049730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hobbs, Helen H.
 ; APPLICANT: Shan, Bei
 ; APPLICANT: Barnes, Robert
 ; APPLICANT: Talarik Inc.
 ; APPLICANT: Board of Regents, The University of Texas System
 ; TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
 ; FILE REFERENCE: 01781-007320US
 ; CURRENT APPLICATION NUMBER: US/09/989, 981A
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/252, 235
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/253, 645
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 673
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: human ABCG8 (hABCGB)
 ; OTHER INFORMATION: human ABCG8 (hABCGB)

US-09-989-981A-8

Query Match 21.0%; Score 697; DB 10; Length 673;
 Best Local Similarity 28.9%; Pred. No. 2.2e-57; Matches 187; Conservative 124; Mismatches 241; Indels 96; Gaps 16; Matches 187; Connervative 124; Mismatches 241; Indels 96; Gaps 16;

Qy 8 TPGGSMGLQNRGQSSELEGAPAT-APPHSLGILHASYSYSHRV-PRWD-ITSRCQW 64
 Db 16 TPGDTSGLQDRLFSSESNSLYPTSGQPNLTVRDLYQVNLQWPEQLAQPKPW 75
 Qy 65 TROI-----LKDVSILYESQIMCILGSSGSKTLLDAMSGRIGRAGTF-LGEVYV 115
 Db 76 TSPSQNSELIGIONLISFKRSQMLAATIGSSGGGRASSLVDVTRG-QHGGKIKSGQIWI 134
 Qy 16 NGRALRREQFQDCFSYVQSDTLLSITRETHYHALLAI-RRGNPQSFQKVEAYMNE 174
 Db 135 NGQSPSPQVLVRKCVAHVROHNLQPLNPTVRETLAFQAMRLPRTFSQARQDRKVEDVIA 194
 Qy 175 NGQSPSPQVLVRKCVAHVROHNLQPLNPTVRETLAFQAMRLPRTFSQARQDRKVEDVIA 194
 Db 195 LRIROCADPVRGNNYVRQUSGGERRVSVQQLWNPQGILDEPTGIDCMTANQWVL 234
 Qy 235 LVELARRNIVVTHQRSSEFQLDKIALSPGENIFCGPAEMDDPFDNGYPRPEH 294
 Db 255 LSLAKGNRILVLIHOPRSIDFLFDLVLIMTSGTPYLGAQMQVYFTSIGHPC 311
 Qy 295 SNPDPYMDTSVOTOSKEREIEITSKRVQMEAYKKAICHTKLKQIERMKHL---- 348
 Db 315 SNPDPYDVLTSIDRSRQELETREKQSLAFL-----LEKVRDDEFLW 362
 Qy 349 -----KTLN-----VPKURDSDPVFSKQVLLRVRVNLVRNLKAVTRL 390
 Db 363 AETKDLDETCVESSVNDLNCIPSPK-MPAQVQFTTLLRQISNDPFLTLLH 421
 Qy 391 LQNLIMGLLFLFVLRVSNVLKGIAQ---DRVGLAYOFQATPYCQMLNAVNLPFLVR 446
 Db 422 AEACLMWSMIGFLYFG----HGSIOFSMDTAALLMIGALIPNVNLDVSKCYB 475
 Qy 447 AVSDQESDQGLYQKQMMIAYALVLPSSVAMIFSSCYWTLGHLPEVARP---- 499
 Db 476 AMVYELLEDGLYTGPFYFFAKLGEPLPBCAVTYGMPYTLRGLQPLFLHLLV 535
 Qy 500 -----GYSAALIAPHLIGEFLTLLGIVQMNIVNIVSNVWALISIAGVINGGFL 549
 Db 536 WLUVFCCRIMALAAAALLPFTMASFFS-----NAYLNSPYLAG----GFM 577
 Qy 550 RNQEMPFFKISYFTFQKCYCBAIUVNBPFYGLNFTCGSSNVSTIN 597
 Db 578 INLSLWTVPAWISKUSFLRWCSEGMLKIQFSRTYKQPLGNLTAVS 625

RESULT 9
 US-10-090-455-7
 ; Sequence 7 Application US/10090455
 ; Publication No. US20030027259A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Hongyun
 ; TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND USES THEREOF
 ; FILE REFERENCE: 10103-406
 ; CURRENT APPLICATION NUMBER: US/10/090, 455
 ; CURRENT FILING DATE: 2002-01-01
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSBQ for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 673
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: human ABCG8 (hABCGB)

US-10-090-455-7

Query Match 21.0%; Score 637; DB 14; Length 673;
 Best Local Similarity 28.9%; Pred. No. 2.2e-57; Matches 187; Connervative 124; Mismatches 241; Indels 96; Gaps 16; Matches 187; Connervative 124; Mismatches 241; Indels 96; Gaps 16;

Qy 8 TPGGSMGLQNRGQSSELEGAPAT-APPHSLGILHASYSYSHRV-PRWD-ITSRCQW 64
 Db 16 TPGDTSGLQDRLFSSESNSLYPTSGQPNLTVRDLYQVNLQWPEQLAQPKPW 75
 Qy 65 TROI-----LKDVSILYESQIMCILGSSGSKTLLDAMSGRIGRAGTF-LGEVYV 115
 Db 76 TSPSQNSELIGIONLISFKRSQMLAATIGSSGGGRASSLVDVTRG-QHGGKIKSGQIWI 134
 Qy 16 NGRALRREQFQDCFSYVQSDTLLSITRETHYHALLAI-RRGNPQSFQKVEAYMNE 174
 Db 135 NGQSPSPQVLVRKCVAHVROHNLQPLNPTVRETLAFQAMRLPRTFSQARQDRKVEDVIA 194
 Qy 175 LSLSVADLIGNSLGJSTGRVVAQQLQDPKMLFEPPTGIDCMTANQWVL 234

RESULT 14
US-09-405-806-2

Query Match 20.5%; Score 680.5; DB 15; Length 655;
Best Local Similarity 29.2%; Pred. No. 8.1e-56;
Matches 182; Conservative 137; Mismatches 250; Indels 55; Gaps 18;

QY 138 LLSITVTRELYHYALLAARRGNPG-SQKKEVAMWELSLHVADLIGNYSLGGISTG 196
Db 130 VNGTUVRENTLOFSAALRATMTNHEKNERINRVIOGLGDKVADSKVGTQFIRGVSGG 189

QY 197 ERRVSIAMQQLQDPKVMFDEPTTGLDQMTANQIVVILVELARNRIVLTHOPSEL 256
Db 190 ERKTSIGMLITPSILUDDEPTGLOSSTANAVLILKRMKSQGRTISIHOPRSI 249

QY 257 FOLDFKIALISFGENIFCCTPAEMIDFFNDCGPCPEHNSNPFPYMDLTSVDTQ---SK 312
Db 250 FKUDSLLASGRMLPHQPAEALGIFSSAGTCHEAVNPADFFDINGSTAVANR 309

QY 313 ERE-----IETSKR---VOMTISAYKSAICHT-----LKNIERMKHLTKLPMVF 356
Db 310 EDFKATEIEPSKDKPLIEKLAKBYIVNNSFYKETKALHOSGGERKKKTVKESY 369

QY 357 KTKDSDGVSKLGVLIRRNLVYENKLAVITRILQNLNGFL---LFFVLVRVSNLKG 414
Db 370 TT---SFCHQURWWSKSFKNLGNPQASIAQIIVTVVGLVIGAIYFGKNDST--- 421

QY 415 AIQDRVGLQFVGATPTYGMNANLPTURAVSDQESDQGQYQKWMMLAL-HVLP 473
Db 422 GIONRAGVLF-FLTNNQCSFSSVSAVLFYVEKKLTHEYISGYVRVSSYFLGKLSLIP 480

QY 474 FSVVATMIFSSVCYIWTGHLPEVARPGYSAALLAAPHLIGEFTLVLIGIVQNPNIVS 533
Db 481 NRMLSIIFCIVYIMLGKPKADAFVNMFTL---WVAYASMSMALIA3GSUVSVA 537

QY 534 VALLSTAGV--LNGSGFLRNQEMPIFPKISYTFQKCYSEIIVNNEFYGLNFTCGSSN 591
Db 538 TLMMTCFVFMIFPSLVLNLTIASLWSLWQLQFSIPRGFTALQHNEFLGONPCPG--- 594

QY 592 VSUTTNPMCACTQGIFIEKTCG 615
Db 595 LNATGNNPVNAYA-----TCTG 610

RESULT 15
US-09-866-866A-10

Query Match 20.3%; Score 674.5; DB 9; Length 655;
Best Local Similarity 29.0%; Pred. No. 3.1e-55; Matches 181; Conservative 131; Mismatches 251; Indels 55; Gaps 18;

QY 21 SOSSLSGAPATAP--EPMHSGILHASYSVSRVREWWMDITSCROWTQIQLKSVLYE 77
Db 13 SOQNTNGPAPASNDLKAFTGAVSLSPHNCITYRVLKSGLPCKRVEKEILSNINGMK 72

QY 78 SQQQIMCILGSSGSKTILDAMSGRLLGRAGTFLGEVYVNGALRREQFOODCCFSYVQSDT 137

OY	78	SGQIMCIGTGSSGSKTTLDDAMSGRIGRAGTFGLGEVYNGRALRQEOFDCFSYVLSDTI	137
Db	73	PQ-INALIGPTGGKESLSDVAAKRDPSL-LSGUTV	129
OY	138	LISSLTYTRETYLTALAIIRGRNGPG-SFOQKVEAWAEISLISHYADRJTGNSLGG-STG	196
Db	130	WQGTLTIRENQFSALRLATMTINHEKERNRINRTEBGLDKVADSKVGTQ-TRGSGG	189
OY	197	BERRVSTAQOLQDKWMLFDEPTGQDWMQVWILMLKREMSKGRTTIFSIIHOPRSI	249
Db	190	ERKRTSIGMELITDPSLSDLEPTGQDMSSTANAVLWLLKREMSKGRTTIFSIIHOPRSI	256
OY	257	FOLFDKIALFGLFELFCGTGPAEMUDLFFNDGCGYGPPEPHSNPDPYDMDTSVUDQ--SK	312
Db	250	FRLFDSDITLGLASGRJMFHGPQAEALGYFESAGYHETVNNPAPDFFLDINGDTAVANR	309
OY	313	ERB---IENSKR---VQMEISAYKSAICHT---LKNIEERMKHLKTLPLMVPP	356
Db	310	REDPKATEIIEPSKOPKPLIEKLAETYVNNPSYKEVKAELHOLSGGCKCKCTVKEISY	369
OY	357	KIKDPSGVFSKUGVLLRVRVTLVNRKLVITRULQNLIMFLJ---LFLVLRPSRNWK	414
Db	370	TT---SFCHOIWRWRSRSRSPKFLGKQFQASIAQTIVTWTGLVIGAIIYPLKNDST---	421
OY	415	AQDROVGLYKQNGAMPYTGMLAVNLVLPVURAVSDQESODGLYQKQWMLAYAL-HVLP	473
Db	422	GIQNRCAGLPL-FLTTWQCPSSVSVAVLFLWVEKLFIEHYTISGYVRVSSYFLGLKSLDLP	480
OY	474	FSVTATMFSSVYWTGILHPEVARVGYFSALLAAPHLIGEFLTIVLGLIVVNPNINNSV	533
Db	481	NRMPLPSIIFTCIVYFVFMGLKPKGADAPVFMETL--MVAYSASMMALIAQOSVNSVA	537
OY	534	VALLISLGV-IVGSGFLRNTQEMP-PPKPLSYFTPOKSYESEILVNVBNERYGUNFTCGSSN	591
Db	538	TLMTCFVPMIFSGHJLNLTTIASLWSLQYFSPRGFTALQHNERFLGQNCPCG--	594
OY	592	VSVTITNPMCAFTGQDIEKICPG	615
Db	595	LNATGNPNCPNIA-----TGTG	610

Search completed: March 17, 2004, 19:53:51
Job time : 26.0763 secs